

GenCore version 5.1.4-p5-4578  
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On protein - protein search, using sw model

Run on: April 8, 2003, 14:23:22 ; Search time 38 Seconds  
(without alignments) 2955.149 Million cell updates/sec

Title: US-09-001-737-8  
Perfect score: 7653  
Sequence: I-M-A-K-E-I-K-F-S-D-A-R-A-M-V-R-G-V-D.....T-P-A-P-A-M-P-A-G-H-D-P-G-K-M-G-M-G-G 545

Scoring table: BLOSUM2

Gapp 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRREMBL\_21,\*

1: sp\_archeab,\*  
2: sp\_bacteria,\*  
3: sp\_fungi,\*  
4: sp\_human,\*  
5: sp\_invertebrate,\*  
6: sp\_mammal,\*  
7: sp\_mhc,\*  
8: sp\_organelle,\*  
9: sp\_phage,\*  
10: sp\_plant,\*  
11: sp\_rabbit,\*  
12: sp\_virus,\*  
13: sp\_vertebrate,\*  
14: sp\_unclassified,\*  
15: sp\_virus,\*  
16: sp\_bacteriop,\*  
17: sp\_archeap,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2.83	5	89.5	540
2	2.80	89.4	540	2 Q9AET7
3	2.34	88.1	540	16 Q8YV84
4	2.33	87.6	481	2 O3733
5	2.30	87.5	540	2 O3X45
6	2.19	82.4	541	2 Q3EUS5
7	2.18	82.1	542	2 Q9AEP7
8	2.09	85.5	539	2 Q9C20
9	2.01	11.5	539	2 Q8YV84
10	2.00	3.5	75.2	2 Q8YV4
11	1.99	5.5	544	2 O32847
12	1.95	74.5	535	2 Q93G16
13	1.94	73.2	543	2 Q9KJ23
14	1.90	71.5	538	16 Q99SL7
15	1.88	70.9	525	2 Q8VTM6
16	1.87	70.5	525	2 Q8VTM8

RESULTS

RESULT 1

ID	Q9AME7	PRELIMINARY:	PRT:	540 AA.
AC	Q9AME7			
DT	01-JUN-2001	(T=EMBLrel. 17, last sequence update)		
DT	01-JUN-2001	(T=EMBLrel. 17, last annotation update)		
DE	60 kDa chaperonin (Protein Cpn60). (GroEL protein).			
OS	Streptococcus agalactiae.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococaceae; Streptococcus.			
OX	NCBL-TaxID1311.			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RA	Jwo-Farn C.;	"Cloning, sequencing, and characterization of 60 kDa chaperonin gene from Streptococcus agalactiae,"		
RT	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
RT	-!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).			
CC	-!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).			
CC	-!- SIMILARITY: BELONGS TO THE CHAPERONIN (CHSP60) FAMILY.			
DR	EMBL: AF322222; ARK12938; 1; -;			
DR	HSSP: P06119; IGRL			
DR	InterPro: IPR001844; Chaperin_Cpn60.			
DR	InterPro: IPR002423; Cpn60/TCP-1.			
DR	Pfam: PF00118; Cpn60_TCP1; 1.			
DR	PRINTS: PRO0298; CHAPERONIN60.			
DR	PRINTS: PRO03034; TCOMPLEXTCP1.			
DR	PROSITE: PS00296; CHAPERONINS_CPN60; 1.			
KW	ATP-binding; Chaperone.			
SEQUENCE	540 AA; 57287 MW;	F392085FCF919DD1 CRC64;		

Query Match Similarity 89.5%; Score 2383.5; DB 2; Length 540; Best Local Similarity 89.7%; Pred. No. 2.1e-105; Matches 486; Conservative 25; Mismatches 28; Indexes 3; Gaps 2;

OY	1 MAKEIKFSAVARAMYRGVDMILADTVKVTGPKGRNVVLEKAFGSPLINDGUTIAKEIE 60	Db	1 MAKOKFSAVARVGVDILADTVKVTGPKGRNVVLEKAFGSPLINDGUTIAKEIE 60
Db	1 MAKOKFSAVARVGVDILADTVKVTGPKGRNVVLEKAFGSPLINDGUTIAKEIE 60	Db	1 MAKOKFSAVARVGVDILADTVKVTGPKGRNVVLEKAFGSPLINDGUTIAKEIE 60
OY	61 LEDIFENNGAKLUSSEVASKTDINGDGTTATWLTQATWESLKNTAGANGPIGTRRGIE 120	Db	61 LEDIFENNGAKLUSSEVASKTDINGDGTTATWLTQATWESLKNTAGANGPIGTRRGIE 120
Db	61 LEDIFENNGAKLUSSEVASKTDINGDGTTATWLTQATWESLKNTAGANGPIGTRRGIE 120	Db	61 LEDIFENNGAKLUSSEVASKTDINGDGTTATWLTQATWESLKNTAGANGPIGTRRGIE 120
OY	181 METELEVVEGMDRGLSQYMDTNEMKADELNPFLIDKKSNQDIPPLEEVLK 240	Db	181 METELEVVEGMDRGLSQYMDTNEMKADELNPFLIDKKSNQDIPPLEEVLK 240
Db	181 METELEVVEGMDRGLSQYMDTNEMKADELNPFLIDKKSNQDIPPLEEVLK 240	Db	181 METELEVVEGMDRGLSQYMDTNEMKADELNPFLIDKKSNQDIPPLEEVLK 240
OY	241 TNRPLLIADDVGGEALPTLVNKIRGTFNVAKPFGDRRKAMEDIAITLGTVIT 300	Db	241 TNRPLLIADDVGGEALPTLVNKIRGTFNVAKPFGDRRKAMEDIAITLGTVIT 300
Db	241 TNRPLLIADDVGGEALPTLVNKIRGTFNVAKPFGDRRKAMEDIAITLGTVIT 300	Db	241 TNRPLLIADDVGGEALPTLVNKIRGTFNVAKPFGDRRKAMEDIAITLGTVIT 300
OY	301 EDIGLEKDAMTALGOKAKITVORKDSVTVEGSSSEAIANRILNLSOLTTSDPR 360	Db	301 EDIGLEKDAMTALGOKAKITVORKDSVTVEGSSSEAIANRILNLSOLTTSDPR 360
Db	301 EDIGLEKDAMTALGOKAKITVORKDSVTVEGSSSEAIANRILNLSOLTTSDPR 360	Db	301 EDIGLEKDAMTALGOKAKITVORKDSVTVEGSSSEAIANRILNLSOLTTSDPR 360
OY	361 EKIQERLAKLAGGYAVIKVGAFTALKMURBEDALNATRAVEGTVAGGGTALTV 420	Db	361 EKIQERLAKLAGGYAVIKVGAFTALKMURBEDALNATRAVEGTVAGGGTALTV 420
Db	361 EKIQERLAKLAGGYAVIKVGAFTALKMURBEDALNATRAVEGTVAGGGTALTV 420	Db	361 EKIQERLAKLAGGYAVIKVGAFTALKMURBEDALNATRAVEGTVAGGGTALTV 420
OY	421 IEKVAALELEGDDATGRNIVRALKALEPVRQALNAGTESSVVIDKLNNSPAGTAGNATG 480	Db	421 IEKVAALELEGDDATGRNIVRALKALEPVRQALNAGTESSVVIDKLNNSPAGTAGNATG 480
Db	421 IEKVAALELEGDDATGRNIVRALKALEPVRQALNAGTESSVVIDKLNNSPAGTAGNATG 480	Db	421 IEKVAALELEGDDATGRNIVRALKALEPVRQALNAGTESSVVIDKLNNSPAGTAGNATG 480
OY	481 EWMDMKGIDPVKVRSLQNAVASVSLILTEAVANKPEPATPAPAMPAGDGM 540	Db	481 EWMDMKGIDPVKVRSLQNAVASVSLILTEAVANKPEPATPAPAMPAGDGM 540
Db	481 EWMDMKGIDPVKVRSLQNAVASVSLILTEAVANKPEPATPAPAMPAGDGM 540	Db	481 EWMDMKGIDPVKVRSLQNAVASVSLILTEAVANKPEPATPAPAMPAGDGM 540
OY	541 GG : 542	Db	541 GGM : 543
Db	538 GG 539	Db	537 GGM 539
RESULT 2			
DBVTB	PRELIMINARY; PRT; 540 AA.	DB	PRELIMINARY; PRT; 540 AA.
ID	08V758	ID	08V758
AC	08V758;	AC	08V758;
DT	DT 01-MAR-2002 (TREMBREL. 20, Created)	DT	DT 01-MAR-2002 (TREMBREL. 20, Last sequence update)
DT	01-MAR-2002 (TREMBREL. 21, Last annotation update)	DT	01-JUN-2002 (TREMBREL. 21, Last annotation update)
DE	GROEL.	DE	GROEL.
OS	Streptococcus gordoni <sup>1</sup> .	OS	Streptococcus gordoni <sup>1</sup> .
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;	OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
SC	Streptococcaceae; Streptococcus.	SC	Streptococcaceae; Streptococcus.
OX	NCBI_TaxID=1302;	OX	NCBI_TaxID=1302;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N. A.	RP	SEQUENCE FROM N. A.
RC	STRAIN=ATCC1058;	RC	STRAIN=TIGRA;
RA	Teng L.-J., Hsu J.-C.,	RA	MEDLINE=2135709; PubMed=114631915;
RT	*The grotEST of Streptococcus gordoni ATCC 1058.;	RT	Telesh S., Nelson K. E., Paulsen I. T., Eisen J. A., Read T. D., Peterson S., Heidelberg J. F., Deboy R. T., Hart D. H., Dodson R. J., Durkin A. S., Gwinn M., Kolonay J. F., Nelson W. C., Peterson J. D., Durkin A. S., Gwinn M., Kolonay J. F., Nelson W. C., Radune D., Uniyanen L. O., White O., Salzberg S. L., Lewis M. R., Radune D., Holzapfel E., Khouri H., Wolf A. M., Utterback T. R., Hansen C. L., McDonald L., Feldblyum T. V., Argalioli S., Dickinson T., Hickey E. K., Holt I. E., Loftus B. J., Yang P., Smith H. O., Venter J. C., Dougherty B. A., Morrison D. A., Hollingshead S. K., Fraser C. M.;
DR	InterPro: IPR001840; Chaperonin_Cpn60.	DR	Dougherty B. A., Morrison D. A., Hollingshead S. K., Fraser C. M.;
DR	InterPro: IPR002433; Cpn60_TCP-1.	DR	InterPro: IPR002433; Cpn60_TCP-1.
DR	Pfam: PF00118; CPN60_TCP-1.	DR	Pfam: PF00118; CPN60_TCP-1.
DR	PRINTS: PRO028; CHAPERONINO.	DR	PRINTS: PRO028; CHAPERONINO.
DR	PRINTS: PRO034; TCOMPLEXC1.	DR	PRINTS: PRO034; TCOMPLEXC1.
DR	PROSITE: PS00096; CHAPERONINS_CPN60; UNKNOWN <sup>1</sup> .	DR	PROSITE: PS00096; CHAPERONINS_CPN60; UNKNOWN <sup>1</sup> .
SO	SEQUENCE 540 AA: 56769 MW: EA4A7712767CEF39 CRC64:	SO	SEQUENCE 540 AA: 56769 MW: EA4A7712767CEF39 CRC64:
OY	Query Match 89.4%; Score 2380; DB 2; Length 540; Best Local Similarity 88.2%; Pred. No. 3.6e-105; Matches 479; Conservative 39; Mismatches 21; Indels 4; Gaps 1.	OY	Query Match 89.4%; Score 2380; DB 2; Length 540; Best Local Similarity 88.2%; Pred. No. 3.6e-105; Matches 479; Conservative 39; Mismatches 21; Indels 4; Gaps 1.
RESULT 3			
DBVTB	PRELIMINARY; PRT; 540 AA.	DB	PRELIMINARY; PRT; 540 AA.
ID	097NV4	ID	097NV4
AC	097NV4;	AC	097NV4;
DT	DT 01-OCT-2001 (TREMBREL. 18, Created)	DT	DT 01-OCT-2001 (TREMBREL. 18, Last sequence update)
DT	DT 01-MAR-2002 (TREMBREL. 20, Last annotation update)	DT	DT 01-MAR-2002 (TREMBREL. 20, Last annotation update)
DE	Chaperonin, 60 kDa (GROEL).	DE	Chaperonin, 60 kDa (GROEL).
GN	SPI1966.	GN	SPI1966.
OS	Streptococcus pneumoniae.	OS	Streptococcus pneumoniae.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;	OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
SC	Streptococcaceae; Streptococcus.	SC	Streptococcaceae; Streptococcus.
OX	NCBI_TaxID=1313;	OX	NCBI_TaxID=1313;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N. A.	RP	SEQUENCE FROM N. A.
RC	STRAIN=TIGRA;	RC	STRAIN=TIGRA;
RA	MEDLINE=2135709; PubMed=114631915;	RA	MEDLINE=2135709; PubMed=114631915;
RT	Telesh S., Nelson K. E., Paulsen I. T., Eisen J. A., Read T. D., Peterson S., Heidelberg J. F., Deboy R. T., Hart D. H., Dodson R. J., Durkin A. S., Gwinn M., Kolonay J. F., Nelson W. C., Peterson J. D., Durkin A. S., Gwinn M., Kolonay J. F., Nelson W. C., Radune D., Uniyanen L. O., White O., Salzberg S. L., Lewis M. R., Radune D., Holzapfel E., Khouri H., Wolf A. M., Utterback T. R., Hansen C. L., McDonald L., Feldblyum T. V., Argalioli S., Dickinson T., Hickey E. K., Holt I. E., Loftus B. J., Yang P., Smith H. O., Venter J. C., Dougherty B. A., Morrison D. A., Hollingshead S. K., Fraser C. M.;	RT	Telesh S., Nelson K. E., Paulsen I. T., Eisen J. A., Read T. D., Peterson S., Heidelberg J. F., Deboy R. T., Hart D. H., Dodson R. J., Durkin A. S., Gwinn M., Kolonay J. F., Nelson W. C., Peterson J. D., Durkin A. S., Gwinn M., Kolonay J. F., Nelson W. C., Radune D., Uniyanen L. O., White O., Salzberg S. L., Lewis M. R., Radune D., Holzapfel E., Khouri H., Wolf A. M., Utterback T. R., Hansen C. L., McDonald L., Feldblyum T. V., Argalioli S., Dickinson T., Hickey E. K., Holt I. E., Loftus B. J., Yang P., Smith H. O., Venter J. C., Dougherty B. A., Morrison D. A., Hollingshead S. K., Fraser C. M.;
RA	Dougan G., Young A., Wright J. A., Dugourd D. F.,	RA	Dougan G., Young A., Wright J. A., Dugourd D. F.,
RA	Science 293:498-506(2001).	RA	Science 293:498-506(2001).
RT	[2] SEQUENCE FROM N. A.	RT	[2] SEQUENCE FROM N. A.
RC	STRAIN=ESP14;	RC	STRAIN=ESP14;
RA	Molecular chaperones/chaperonin-encoding stress genes groEL and groES	RA	Molecular chaperones/chaperonin-encoding stress genes groEL and groES

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3

RT	and their use as antimicrobial targets."
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AE001482; AAR75796; 1;
DR	AF325449; AAL5597; 1; -;
TIGR	SP1306; -;
DR	InterPro: IPR001844; Chaperonin_Cpn60.
DR	InterPro: IPR02433; Cpn60_TCPI-1.
DR	Pfam: PF00118; Cpn60_TCPI_1.
PRINTS	PR028; CHAPERONIN60.
DR	PRINTS: PR0304; TCOMPLEXTCPI.
DR	PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW	Complete proteome.
SQ	SEQUENCE: 540 AA; 57095 MW; EBA6CB1960CD894C CRC64;
Query	Match 88.1%; Score 2347; DB 16; Length 540;
Best Local Similarity	87.8%; Pred. No. 1.3e-103;
Matches	477; Conservative 34; Mismatches 28; Indels 4; Gaps 1;
OY	1 MAKEIKFSNDARARAMTRGVDMLADTVKTYLGPKRNVLEKAFGSPLINGTYIAKEIE 60
Db	1 MSKEIKFSSDANSAMSYRQVGDILADTVKTYLGPKRNVLEKAFGSPLINGTYIAKEIE 60
OY	61 LEDHDEENNGAKVSEASKNDAGDTTATVTOAIVHESGLKNTAGANPIGIRGIE 120
Db	61 LEDHEENNGAKVSEASKNDAGDTTATVTOAIVHESGLKNTAGANPIGIRGIE 120
OY	121 TATAAAVEALKAIQAQVAVVASSRSEKVYIEMMERVGNDVYTIESRG 180
Db	121 TATAAAVEALKAIQAQVAVVASSRSEKVYIEMMERVGNDVYTIESRG 180
OY	181 METELEVSEGKDFGQLSOMTDNEKKMADLENPLFILIDDKYSNQIDIPLLEVLK 240
Db	181 METELEVSEGKDFGQLSOMTDNEKKMADLENPLFILIDDKYSNQIDIPLLEVLK 240
OY	301 EDGLELKDATTAALGQAKRVTVDKOSTVIEGGNSSEANRNLISQLETTSDDFR 360
Db	301 EDGLELKDATTAALGQAKRVTVDKOSTVIEGGNSSEANRNLISQLETTSDDFR 360
OY	241 TNRPLLIADDGEALPPLVINKRGTNNVAVAKAPFGDKRAMEIDALITGGTIV 300
Db	241 SNRPLLIKADDGEALPPLVINKRGTNNVAVAKAPFGDKRAMEIDALITGGTIV 300
OY	301 EDGLELKDATTAALGQAKRVTVDKOSTVIEGGNSSEANRNLISQLETTSDDFR 360
Db	301 EDGLELKDATTAALGQAKRVTVDKOSTVIEGGNSSEANRNLISQLETTSDDFR 360
OY	181 EKQERLAKLAGGVAVIKVAGTPEALKEMKLREDLNATRAVEEGVIGGGTIV 420
Db	361 EKQERLAKLAGGVAVIKVAGTPEALKEMKLREDLNATRAVEEGVIGGGTIV 420
OY	421 LEKVALEEDGDAYGNVIRALEPVRQIALNAGIEGSVTKLNSPACTGENATG 480
Db	421 LEKVALEEDGDAYGNVIRALEPVRQIALNAGIEGSVTKLNSPACTGENATG 480
OY	481 EWDVKIGIDPVKVTASALONAASVSLILTEAVANKKPPATPAPAMPDMGG 540
Db	481 EWDVKIGIDPVKVTASALONAASVSLILTEAVANKKPPATPAPAMPDMGG 540
OY	541 GGM 543
Db	537 GGM 539
RESULT	4
O33733	PRELIMINARY; PRT; 481 AA.
ID	033733; PRELIMINARY; PRT; 481 AA.
AC	033733; PRELIMINARY; PRT; 481 AA.
DT	01-JAN-1998 (TREMBREL 05, Created)
DT	01-JAN-1998 (TREMBREL 05, Last sequence update)
DT	01-MAR-2002 (TREMBREL 20, Last annotation update)
DE	60 kDa Chaperonin (Protein Cpn60) (GroEL protein).
GROEL	GroEL.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus.
OS	Streptococcus pneumoniae.
GN	Streptococcus pneumoniae.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus.
OX	NBRL-TAXID=1313;
(1)	
RESULT	5
O9X4R5	SEQUENCE FROM N-A.
ID	09X4R5
AC	09X4R5
DT	01-NOV-1999 (TREMBREL 12, Created)
DT	01-NOV-1999 (TREMBREL 12, Last sequence update)
DT	01-MAR-2002 (TREMBREL 20, Last annotation update)
DE	60 kDa chaperonin (Protein Cpn60) (GroEL protein).
GROEL	GroEL.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus.
OS	NBRL-TAXID=1313;
(1)	
RP	SEQUENCE FROM N-A.
RC	STRAIN=SEROTYPE M49.
RA	Pohl B. Pobieski A., Zarges I.;
RL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC	-I FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
CC	-I SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
CC	-I SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR	EMBL: X99236; CAA61520; 1;
DR	HSSP: P06119; IGRL
DR	InterPro: IPR01844; Chaperonin_Cpn60.
DR	InterPro: IPR002423; Cpn60_TCPI-1.
PFAM	PF00118; Cpn60_TCPI_1.
PRINTS	PR0298; CHAPERONIN60.
DR	PRINTS: PR0304; TCOMPLEXC1.
PROSITE	PS00296; CHAPERONINS_CPN60; 1.
DR	ATP-binding; Chaperone.
FT	NON_TER 1 1
SO	SEQUENCE: 481 AA; 50496 MW; FA80B997CA7BD11 CRC64;
Query	Match 87.6%; Score 2333; DB 2; Length 481;
Best Local Similarity	99.4%; Pred. No. 5.1e-103;
Matches	477; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY	63 DIRENGAKVSEVASTNDAGDTTATVTOAIVHESGLKNTAGANPIGIRGIE 122
Db	1 DIRENGAKVSEVASTNDAGDTTATVTOAIVHESGLKNTAGANPIGIRGIE 122
OY	123 TATAAAVEALKAIQAQVAVVASSRSEKVYIEMMERVGNDVYTIESRG 182
Db	61 TATAAAVEALKAIQAQVAVVASSRSEKVYIEMMERVGNDVYTIESRG 182
OY	183 TLEEVSEGKDFGQLSOMTDNEKKMADENPLTDKVSNQIDIPLLEVLKTN 242
Db	121 TLEEVSEGKDFGQLSOMTDNEKKMADENPLFILDKVSNQIDIPLLEVLKTN 180
OY	243 RPLIADDVGALPPLVINKRGTNNVAVAKAPFGDKRAMEIDALITGGTIV 302
Db	61 TATAAAVEALKAIQAQVAVVASSRSEKVYIEMMERVGNDVYTIESRG 120
OY	303 IGLELKDATTAALGQAKRVTVDKOSTVIEGGNSSEANRNLISQLETTSDDFR 362
Db	241 IGLELKDATTAALGQAKRVTVDKOSTVIEGGNSSEANRNLISQLETTSDDFR 360
OY	363 LOERLAKLAGGVAVIKVAGTPEALKEMKLREDLNATRAVEEGVIGGGTIV 422
Db	301 LOERLAKLAGGVAVIKVAGTPEALKEMKLREDLNATRAVEEGVIGGGTIV 360
OY	423 LEKVALEEDGDAYGNVIRALEPVRQIALNAGIEGSVTKLNSPACTGENATG 482
Db	361 LEKVALEEDGDAYGNVIRALEPVRQIALNAGIEGSVTKLNSPACTGENATG 482
OY	483 VDMIKIGIDPVKVTASALONAASVSLILTEAVANKKPPATPAPAMPDMGG 542
Db	421 VDMIKIGIDPVKVTASALONAASVSLILTEAVANKKPPATPAPAMPDMGG 480

RP SEQUENCE FROM N.A.  
 RC STRAIN=CP120;  
 RA Kim S.N., Lee J.Y., Kim S.W., Choi I.H., Rhee D.K.;  
 RT "groEST sequences in *Streptococcus pneumoniae*";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.  
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
 CC CONDITIONS (BY SIMILARITY).  
 CC -I- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 DR -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
 EMBL: AF117441; AAD23455; 1;  
 HSP: P06139; 1CPL;  
 DR InterPro: IPR001844; Chaperonin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60/TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1;  
 DR PRINTS: PR0039; CHAPERONIN60.  
 DR PROSITE: PS00296; CHAPERONINS\_CPN60; 1.  
 DR ATP-binding; Chaperone.  
 KW SQ SEQUENCE FROM N.A.  
 Query Match 87.5%; Score 2330; DB 2; Length 540;  
 Best Local Similarity 87.1%; Pred. No. 8.3e+103; Mismatches 473; Conservativeness 36; Indels 7; Gaps 1;  
 Matches 473; Conservative 36; Mismatches 30; Indels 4; Gaps 1;  
 QY 1 MAKEIKFSDADARMARYGVDMLADTVKVTGKGGRNVLKEKGSPPLITNDGYTAKIEF 60  
 Db 1 MAKEIKFSDADARMARYGVDMLADTVKVTGKGGRNVLKEKGSPPLITNDGYTAKIEF 60  
 QY 61 LEDHENNGAKLVSEASKTNDIASEDTTATVLTQAHESGKNTAGANPIRGIE 120  
 Db 61 LEDHENNGAKLVSEASKTNDIASEDTTATVLTQAHESGKNTAGANPIRGIE 120  
 QY 121 TATAFAVEALKAIQPVSKKEAIAQAVAYSSSEKVGTYESEMERVKGVTEESRG 180  
 Db 121 TATAFAVEALKAIQPVSKKEAIAQAVAYSSSEKVGTYESEMERVKGVTEESRG 180  
 QY 181 METELEVSEGKDFGVLISQYNTDKVNSNODILPLEEVLK 240  
 Db 181 METELEVSEGKDFGVLISQYNTDKVNSNODILPLEEVLK 240  
 QY 241 TNRPLLIADDVGELPLTVLKIRGTFVVAVKARGFGDRRKAMLEDIALTGTVIT 300  
 Db 241 SNRPLLIADDVGELPLTVLKIRGTFVVAVKARGFGDRRKAMLEDIALTGTVIT 300  
 QY 301 EDGLELKDATTAGQAKITVDDSTIVGGSSSEIANRALKSSELETTSDPDR 360  
 Db 301 EDGLELKDATTAGQAKITVDDSTIVGGSSSEIANRALKSSELETTSDPDR 360  
 QY 361 EKLOERLAKLAGGVAVKGAETELEMKLRIEDALNTRAAVEGIVAGGTALIV 420  
 Db 361 EKLOERLAKLAGGVAVKGAETELEMKLRIEDALNTRAAVEGIVAGGTALIV 420  
 QY 421 IEKVAALEELDDATGRTVIRAKLDEPRTQALNGYESWVDKKNSPAGTGFNAATG 480  
 Db 421 IPEATELTDGEGATDTGMRVIRAKLDEPRTQALNGYESWVDKKNSPAGTGFNAATG 480  
 QY 481 EWMDIKGIDPPVKTSLQNLQASVASLILITTAWANKKEPATPAPMAGMDPMM 540  
 Db 481 EWMDIKGIDPPVKTSLQNLQASVASLILITTAWANKKEPATPAPMAGMDPMM 540  
 QY 541 GGM 543  
 Db 537 GGM 539  
 RESULT 6  
 Q93E65 PRELIMINARY; PRT; 541 AA.  
 ID Q93E65; PRELIMINARY; PRT; 542 AA.  
 AC 01-DBC-2001 (T-EMBLrel. 19, created)  
 DT 01-DBC-2001 (T-EMBLrel. 19, last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE GROUP.  
 GN R03L.  
 OS Enterococcus faecalis (*streptococcus faecalis*).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Enterococcaceae; Enterococcus.  
 OX NCBI\_TAXID=131;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TCC 29212;  
 RX MEDLINE=21417441; PUBMED=11526171;  
 RA Teng L.J., Hsieh P.R., Wang Y.H., Lin H.M., Luh K.T., Ho S.W.;  
 RT "Determination of *Enterococcus faecalis* groESL Full-Length Sequence and Application for Species Identification";  
 RL J. Clin. Microbiol. 39:3326-3331(2001).  
 DR EMBL: AF35103; AL04033.1;  
 DR InterPro: IPR01844; Chaperonin\_Cpn60.  
 DR InterPro: IPR002423; Cpn60/TCP-1.  
 DR Pfam: PF00118; Cpn60\_TCP1;  
 DR PROSITE: PS00296; CHAPERONINS\_CPN60; UNKNOWN\_1.  
 DR ATP-binding; Chaperone.  
 KW SQ SEQUENCE FROM N.A.  
 Query Match 82.4%; Score 2194; DB 2; Length 541;  
 Best Local Similarity 81.7%; Pred. No. 2.3e+36; Mismatches 445; Conservativeness 46; Indels 6; Gaps 46; Mismatches 48; Indels 6; Gaps 1;  
 QY 1 MAKEIKFSDADARMARYGVDMLADTVKVTGKGGRNVLKEKGSPPLITNDGYTAKIEF 60  
 Db 1 MAKEIKFSDADARMARYGVDMLADTVKVTGKGGRNVLKEKGSPPLITNDGYTAKIEF 60  
 QY 61 LEDHENNGAKLVSEASKTNDIASEDTTATVLTQAHESGKNTAGANPIRGIE 120  
 Db 61 LEDHENNGAKLVSEASKTNDIASEDTTATVLTQAHESGKNTAGANPIRGIE 120  
 QY 121 TATAFAVEALKAIQPVSKKEAIAQAVAYSSSEKVGTYESEMERVKGVTEESRG 180  
 Db 121 TATAFAVEALKAIQPVSKKEAIAQAVAYSSSEKVGTYESEMERVKGVTEESRG 180  
 QY 181 METELEVSEGKDFGVLISQYNTDKVNSNODILPLEEVLK 240  
 Db 181 METELEVSEGKDFGVLISQYNTDKVNSNODILPLEEVLK 240  
 QY 241 TNRPLLIADDVGELPLTVLKIRGTFVVAVKARGFGDRRKAMLEDIALTGTVIT 300  
 Db 241 SNRPLLIADDVGELPLTVLKIRGTFVVAVKARGFGDRRKAMLEDIALTGTVIT 300  
 QY 301 EDGLELKDATTAGQAKITVDDSTIVGGSSSEIANRALKSSELETTSDPDR 360  
 Db 301 EDGLELKDATTAGQAKITVDDSTIVGGSSSEIANRALKSSELETTSDPDR 360  
 QY 361 EKLOERLAKLAGGVAVKGAETELEMKLRIEDALNTRAAVEGIVAGGTALIV 420  
 Db 361 EKLOERLAKLAGGVAVKGAETELEMKLRIEDALNTRAAVEGIVAGGTALIV 420  
 QY 421 IEKVAALEELDDATGRTVIRAKLDEPRTQALNGYESWVDKKNSPAGTGFNAATG 480  
 Db 421 IPEATELTDGEGATDTGMRVIRAKLDEPRTQALNGYESWVDKKNSPAGTGFNAATG 480  
 QY 481 EWMDIKGIDPPVKTSLQNLQASVASLILITTAWANKKEPATPAPMAGMDPMM 540  
 Db 481 EWMDIKGIDPPVKTSLQNLQASVASLILITTAWANKKEPATPAPMAGMDPMM 540  
 QY 541 GGMG 545  
 Db 536 -GMGG 539  
 RESULT 7  
 Q9AEP7 PRELIMINARY; PRT; 542 AA.  
 ID Q9AEP7; PRELIMINARY; PRT; 542 AA.  
 AC 01-JUN-2001 (T-EMBLrel. 17, Created)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)



OY	481	EWWDWMTGIDPDKVYRVSALQNAASVASLILTEAVANKREPATPAPMPAGMDPM-	539	OY	421	IEKVALELEGDDATCRNIVURALESPVUQIALNAGESWVDKLNSPAGTGNTG	480	
Db	481	EWWDWMTGIDPDKVYRVSALQNAASVASLILTEAVANKREPATPAPMPAGMDPM-	533	Db	421	YNKTAATIREGSDBATGVKVLVRARIEBPVQIQANAGLEGSVVIRLSEKGICFGNAAATG	480	
OY	540	-MGGM 543		OY	481	EWWDWMTGIDPDKVYRVSALQNAASVASLILTEAVANKREPATPAPMPAGMDPM-	539	
Db	534	DMGGM 538		Db	481	EWWDWMTGIDPDKVYRVSALQNAASVASLILTEAVANKREPATPAPMPAGMDPM-	533	
	RESULT 9				Db	540	-MGGM 543	
	Q8VV84	PRELIMINARY;	PRT:		Db	534	DMGGM 538	
ID	Q8VV84;							
AC								
DT	01-MAR-2002 (TREMBLrel. 20, Created)							
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)							
DE	GROEL.							
GN								
OS	Bacillus thermoglucosidasius							
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;							
OC	Geobacillus							
OC	NCBI_TaxID=1426;							
OX								
RN								
RP	SEQUENCE FROM N.A.							
RX	STRAIN=TREMBL006;							
RA	Medline=2823196; PubMed=11814128;							
RT	*Oligo1,6-glucosidase from a thermophile, <i>Bacillus</i> sp., strain K1006, was efficiently produced by combinatorial expression of GroEL in <i>Escherichia coli</i> ;"							
RL	Biochem. Appl. Biochem. 35:35-43(2002).							
DR	EMBL: AB025944; BAB991_1;							
DR	InterPro: IPR01844; Chaperonin_Cpn60.							
DR	InterPro: IPR002433; Cpn60_TCP1.							
DR	Pfam: PF00118; Cpn60_TCP1.							
DR	PRINTS: PRO0228; CHAPERONINGO.							
DR	PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.							
DR	SEQUENCE 539 AA; 57192 MW; 7C6BB18FF0C67B5 CRC64;							
Query Match	75.5%; Score 2011.5; DB 2; Length 539;							
Best Local Similarity	74.7%; Pred. No. 2.4e-87; Mismatches 67; Indels 9; Gaps 2;							
Matches 407; Conservative 62; MisMatches 67; Indels 9; Gaps 2;								
OY	1 MAKEIKFSDARAAVRYGVMLADTVKTYGPKGRVYKLEAFGSPPLITNDGVITAKEI 60							
Db	1 MAKEIKFSEARRAMLRGVDKLAADVTVGPKGRVYKLEAFGSPPLITNDGVITAKEI 60							
OY	121 TATATAVEALKAIQPVSGKEIAQVAVANSRSRSEKVKVEYISeamerGNGDVTIERSRG 180							
Db	121 TATATAVEALKAIQPVSGKEIAQVAVANSRSRSEKVKVEYISeamerGNGDVTIERSRG 180							
OY	181 METELEVYEGMDFRGYLSQMYTDKVKYADLENPLITDKVSNIQDILPLEEVLK 240							
Db	181 METELEVYEGMDFRGYLSQMYTDKVKYADLENPLITDKVSNIQDILPLEEVLK 240							
OY	241 TRPLLIADYDGEALPTLVNKTKRGTGKFKRMRKEDAILTGGTVIT 300							
Db	241 OCKPLLIADYDGEALPTLVNKTKRGTGKFKRMRKEDAILTGGTVIT 300							
OY	301 EDGIGELKDQATMVGQAKITDVKOSTVIVESSGSEATANRALKSOLETTSDDR 360							
Db	301 EDGIGELKDQATMVGQAKITDVKOSTVIVESSGSEATANRALKSOLETTSDDR 360							
OY	361 EKLQERLAKLAGGAVAVIKGAPTEALKENKLRIEDALNATRAAVEGIVAGGGTALTV 420							
Db	361 EKLQERLAKLAGGAVAVIKGAPTEALKENKLRIEDALNATRAAVEGIVAGGGTALTV 420							
OY	421 QGPPLLIADYDGEALPTLVNKTKRGTGKFKRMRKEDAILTGGTVIT 300							
Db	421 QGPPLLIADYDGEALPTLVNKTKRGTGKFKRMRKEDAILTGGTVIT 300							

QY 301 EDIGLEKDATMAGQAKITVDKUSTVIEGGSSEIANRILIKSLETTISDFR 360  
 :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 301 BELGBELISTTASLGRASKVWTKNTTVEGAGDDDRKARINORAQLEETTSDFR 360  
 QY 361 EKLOERLAKLAGGVAVIKVGAPTEAKMKTIEDLNATRAVERGIVGGPALTIV 420  
 Db 361 EKLOERLAKLAGGVAVIKVGAPTEAKMKTIEDLNATRAVERGIVGGPALTIV 420  
 QY 421 TEKYAALLEGODATGRNVRALERPVRIALANAGEGSVYDQLKNSPAGTFRNATG 480  
 Db 421 YSKVAALEAGEDEATGVKIVLRAIERPVQIARONAGLEGSVYDQLKNSPAGTFRNATG 480  
 QY 481 EWDMDKGTIDPVKVTRSLQNAASVASLITTEAVVANKPEPATPAPAMPDPN- 539  
 Db 481 EWMVIAEGIVDVKYTRSLQNAASVAMFLTEAVVADKPEE-----NKGNNGMP 533  
 QY 540 -MGGM 543  
 Db 534 DMGGM 538

RESULT 11

ID QJ2847 PRELIMINARY; PRT; 544 AA.  
 AC 032847;  
 DT 01-JAN-1998 (TREMBREL 05, Created)  
 DT 01-MAR-2002 (TREMBREL 20, Last sequence update)  
 DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).

GN GROEL  
 OS Lactobacillus zae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Lactobacillaceae; Lactobacillus;  
 OX NCBI-TAXID=57037;  
 RN [1]  
 RP SEQUENCE FROM N A.

RA Murphy C.M., Chassy B.M.;  
 RT "Molecular Characterization of the Heat-Shock Regulated groEL operon  
 of Lactobacillus zae,"  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
 PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS.  
 CC CONDITIONS (BY SIMILARITY).  
 CC - SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
 CC 7 SUBUNITS (BY SIMILARITY).  
 CC - SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
 DR EMBL: AF010281; AAC66326.1;  
 DR HSSP: B06137; FGRL;  
 DR InterPro: IPR01844; Chaperin\_Cpn60.  
 DR InterPro: IPR02423; Cpn60\_TCP-1.  
 DR Pfam: PF00118; cpn60\_TCP1; 1.  
 DR PRINTS: PRO0298; CHAPERONIN60.  
 DR PRINTS: PRO034; COMPLEXTCP1.  
 DR PROSITE: PS00296; CHAPERONINS\_CPN60; 1.  
 KW ATP-binding; Chaperone.  
 SQ SEQUENCE: 544 AA; 57428 MW; AA2F54F4AC2A1AF CRC64;

Query Match 75.1%; Score 1999.5; DB 2; Length 544;  
 Best Local Similarity 74.1%; Pred. No. 3.8e-87; Gaps 2;  
 Matches 404; Conservative 64; Mismatches 74; Indels 3; Gaps 2;

QY 1 MAKEIKFSADARAAMVYDMLADWVTLGKGKRNWLEKAGSPPLITNDGTYIAKEIE 60  
 Db 1 MAKIKFSEADARAAMVYDMLADWVTLGKGKRNWLEKAGSPPLITNDGTYIAKEIE 60  
 QY 1 LEDPFEMGAKLKVSEVSKTDIAGDTTAVLVTQAVHEGKNTAGANPCTGIRGIE 120  
 Db 61 LEDPFEMGAKLKVSEVSKTDIAGDTTAVLVTQAVHEGKNTAGANPCTGIRGIE 120  
 QY 61 LEDHENNGAKLVAEVSKTDIAGDTTAVLVTQAVHEGKNTAGANPCTGIRGIE 120  
 Db 61 TATATAVAKATAQPVSGREATQAVAVASSERSEKVGTYSEBAMERVENDGVITEESG 180  
 QY 121 TATATAVAKATAQPVSGREATQAVAVASSERSEKVGTYSEBAMERVENDGVITEESG 180  
 Db 117 QATQKAEVOLONSTPESIATVQEVSESSKGKQSYIADAMKYENGVITDSEG 176  
 QY 181 METELEVSEGMDRGYLSQLMVDNEKMDENPFLITDKVSNIQDILPLLEEVLK 240

Db 121 KATKAADELHKISKHNGKKEIAOVASYSSNTENGSLIADMVKHGTVITESKG 180  
 QY 181 METELEVSEGMDRGYLSQLMVDNEKMDENPFLITDKVSNIQDILPLLEEVLK 240  
 Db 181 IDPESLVSEGMDRGYLSQLMVDNEKMDENPFLITDKVSNIQDILPLLEEVLK 240  
 QY 241 TNPLPLIADDVGEGALPTLVNLKIRGTVNVAVAPGSGDRRKAMLEDIAITGGVIT 300  
 Db 241 OGKALLIADDVAGELALPTLVNLKIRGTVNVAVAPGSGDRRKAMLEDIAITGGVIT 300  
 QY 301 EDIGLEKDATMAGQAKITVDKUSTVIEGGSSEIANRILIKSLETTISDFR 360  
 Db 301 SDGLDLDKDTKLEOGRAGKTVPRNTIVDGSKDIAERVNITKQIDDTTSDFR 360  
 QY 361 EKLOERLAKLAGGVAVIKVGAPTEAKMKTIEDLNATRAVERGIVGGTALIV 420  
 Db 361 EKLOERLAKLAGGVAVIKVGAPTEAKMKTIEDLNATRAVERGIVGGTALIV 420  
 QY 421 TEKYAALLEGODATGRNVRALERPVRIALANAGEGSVYDQLKNSPAGTFRNATG 480  
 Db 421 LPVAVALKEGDVQTVGINIVLRAEPPQTAENAGCGSIVVEOLKKKOGVGYNA 480  
 QY 481 EWDMDKGTIDPVKVTRSLQNAASVASLITTEAVVANKPEPATPAPAMPDPN- 539  
 Db 538 AGMGG 542

RESULT 12

ID Q33GT6 PRELIMINARY; PRT; 535 AA.  
 AC 093GTM  
 DT 093GTM;  
 DT 01-DEC-2001 (TREMBREL 19, Created)  
 DT 01-MAR-2002 (TREMBREL 20, Last sequence update)

GN Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Enterococcaceae; Tetragenococcus;  
 OX NCBI-TAXID=51669;  
 RN [1]  
 RP SEQUENCE FROM N A.  
 RA Fukuda D., Watanabe M., Aso Y., Sonomoto K., Ishizaki A.;  
 RT "The groEL operon of halophilic lactic acid bacterium Tetragenococcus  
 halophilus,"  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB073399; BAB77061.1;  
 DR InterPro: IPR02423; Cpn60\_TCP-1.  
 DR Pfam: PF00118; cpn60\_TCP1; 1.  
 DR KW ATP-binding; Chaperone.  
 SQ SEQUENCE: 535 AA; 56893 MW; D9FF681CD3A4D17C CRC64;

Query Match 74.5%; Score 1985; DB 2; Length 535;  
 Best Local Similarity 73.5%; Pred. No. 1.8e-86; Gaps 2;  
 Matches 396; Conservative 73; Mismatches 58; Indels 12; Gaps 2;

QY 1 MAKEIKFSADARAAMVYDMLADWVTLGKGKRNWLEKAGSPPLITNDGTYIAKEIE 60  
 Db 1 MAKIKFSEADARAAMVYDMLADWVTLGKGKRNWLEKAGSPPLITNDGTYIAKEIE 60  
 QY 1 LEDPFEMGAKLKVSEVSKTDIAGDTTAVLVTQAVHEGKNTAGANPCTGIRGIE 120  
 Db 61 LEDPFEMGAKLKVSEVSKTDIAGDTTAVLVTQAVHEGKNTAGANPCTGIRGIE 120  
 QY 121 TATATAVAKATAQPVSGREATQAVAVASSERSEKVGTYSEBAMERVENDGVITEESG 180  
 Db 117 QATQKAEVOLONSTPESIATVQEVSESSKGKQSYIADAMKYENGVITDSEG 176  
 QY 181 METELEVSEGMDRGYLSQLMVDNEKMDENPFLITDKVSNIQDILPLLEEVLK 240

RESULT 13  
 ID QKJ23 PRELIMINARY; PRT: 543 AA.  
 AC O9K123;  
 DT 01-OCT-2000 (TREMBREL, 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBREL, 20, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).  
 GN GROEL.  
 OS Lactobacillus johnsonii.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Lactobacillaceae; Lactobacillus.  
 RN NCBI\_TAXID=33059;  
 RP [1]  
 SEQUENCE FROM N.A.  
 RX STRAIN=VPI 1108;  
 MEDLINE-991859; PubMed=10388700;  
 RT "The groEL chaperon operon of *Lactobacillus johnsonii*.";  
 RL Environ. Microbiol. 65:3041(1999).  
 CC -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).  
 CC -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
 EMBL: AF214488; ARFP7593; 1; -.  
 DR HSSP: P06139; IGR1.  
 DR InterPro: IPR01844; Chaperonin\_Cpn60.  
 DR InterPro: IPR02433; Cpn60\_TCP-1.  
 PRTM: PF00118; Cpn60\_TCP1; 1.  
 PRTM: PRO028; CHAPERONINO.  
 DR PRMTS: PRO0304; TCOMPLEXTCP1.  
 DR PROSITE: PS00296; CHAPERONINS\_CPN60; UNKNOWN\_1.  
 KW ATP-binding; Chaperone.  
 SQ SEQUENCE 543 AA.; 57602 MW; BCE169931CD06338 CRC64;  
 Query Match 73.2%; Score 1948; DB: 2; Length 543;  
 Best Local Similarity 73.1%; Pred No. 1e-84; 2; Mismatches 397; Conservative Matches 62; Gaps 8; Gaps 3; Indels 76;

RESULT 14  
 ID Q9SL7 PRELIMINARY; PRT: 538 AA.  
 AC Q9SL7;  
 DT 01-JUN-2001 (TREMBREL, 17, Created)  
 DT 01-JUN-2001 (TREMBREL, 17, Last sequence update)  
 DT 01-MAR-2002 (TREMBREL, 20, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).  
 GN GROEL OR SAV029 OR SA836.  
 OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699), and  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bactillales;  
 OC Staphylococci.  
 RN NCBI\_TAXID=158878; 158879;  
 RP [1]  
 SEQUENCE FROM N.A.  
 RX SPECIES=S. aureus (strain Mu50), and S. aureus (strain N315); MEDINE-2131953; PubMed=11410146;  
 RA Kuroda M., Onita T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,  
 RA Kanamori M., Matsunaga H., Maruyama A., Murakami H., Hosoya A.,  
 RA Mizutani-Uji Y., Takahashi N.-K., Sawano T., Inoue R.-I., Kaito C.,  
 RA Sekimizu K., Hikavu H., Kubota S., Goto S., Ichibuki J., Shiba T.,  
 RA Kenenisa M., Yamashita A., Oshima K., Furuya K., Yoshino C.,  
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;  
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*," Lancet 357:1225-1240 (2001)  
 CC -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).  
 CC -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).  
 EMBL: AF00364; BAB6911; -.  
 DR AP03135; BAB43161; -.  
 HSSP: P06139; IGR1.  
 DR InterPro: IPR01844; Chaperonin\_Cpn60.  
 DR InterPro: IPR02433; Cpn60\_TCP-1.  
 PRTM: PF00118; cpn60\_TCP1; 1.

